

U9/744852

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SEQUENCE LISTING

<110> FROHBERG, Claus

<120> NUCLEIC ACID MOLECULES ENCODING β -AMYLASE, PLANTS WHICH SYNTHESIZE A MODIFIED STARCH, GENERATION PROCESSES AND USES

<130> 514413-3864

<150> PCT/EP99/05523

<151> 1999-07-30

<150> 198 36 099.1

<151> 1998-07-31

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 1950

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (16)..(1752)

<223> coding sequence beta-amylase

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Ser Gly Thr Ser Leu Thr Ala Glu Thr Gly Gly Val Ser Cys Glu Val	
15 20 25	

ccg gcg aag ggg agt tca gct aca tca gct atg tgg aga aca ccg atg	147
Pro Ala Lys Gly Ser Ser Ala Thr Ser Ala Met Trp Arg Thr Pro Met	
30 35 40	

acg aat tta aaa gta tcg gta caa aaa aca gga act gaa att gac agg	195
Thr Asn Leu Lys Val Ser Val Gln Lys Thr Gly Thr Glu Ile Asp Arg	
45 50 55 60	

gtg tcg ccg tcg ccg tcg ccg ccg atg agt ccg atg atg gga gga gga	243
Val Ser Pro Ser Pro Ser Pro Pro Met Ser Pro Met Met Gly Gly Gly	
65 70 75	

atg cgg ccg gat tta tta gcg tgt caa gcg ttg atg gaa gct cag gta	291
Met Arg Pro Asp Leu Leu Ala Cys Gln Ala Leu Met Glu Ala Gln Val	
80 85 90	

gat gag gta gtt gag aga gaa tat aag gtt agg aat tcg tcg gag aaa	339
Asp Glu Val Val Glu Arg Glu Tyr Lys Val Arg Asn Ser Ser Glu Lys	

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gag	aaa	gga	gtt	ccg	gtg	ttt	gtt	atg	atg	ccg	ttg	gat	agt	gtg	aaa	387
Glu	Lys	Gly	Val	Pro	Val	Phe	Val	Met	Met	Pro	Leu	Asp	Ser	Val	Lys	
	110					115					120					
atg	gat	cat	act	gtg	aat	agg	aag	aag	gcg	atg	aat	gcg	agt	tta	cag	435
Met	Asp	His	Thr	Val	Asn	Arg	Lys	Lys	Ala	Met	Asn	Ala	Ser	Leu	Gln	
125					130					135					140	
gcg	ttg	aag	agc	gcc	ggg	gtg	gaa	ggg	att	atg	atg	gat	gtg	tgg	tgg	483
Ala	Leu	Lys	Ser	Ala	Gly	Val	Glu	Gly	Ile	Met	Met	Asp	Val	Trp	Trp	
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Gly	Leu	Val	Glu	Arg	Asp	Ala	Pro	Gly	Glu	Tyr	Asn	Trp	Gly	Gly	Tyr	
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Ala	Glu	Leu	Met	Glu	Met	Ala	Lys	Lys	His	Gly	Leu	Lys	Val	Gln	Ala	
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gtg	atg	tct	ttc	cat	caa	tgt	ggg	gga	aac	gtc	ggg	gat	tcc	tgc	acg	627
Val	Met	Ser	Phe	His	Gln	Cys	Gly	Gly	Asn	Val	Gly	Asp	Ser	Cys	Thr	
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atc	cct	ctt	cca	agg	tgg	gtt	gtt	gag	gag	atg	gag	aag	gat	cca	gat	675
Ile	Pro	Leu	Pro	Arg	Trp	Val	Val	Glu	Glu	Met	Glu	Lys	Asp	Pro	Asp	
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ctt	gca	tac	aca	gat	cag	tgg	gga	agg	agg	aat	ttt	gaa	tat	gta	tcg	723
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ctt	ggg	tgc	gat	aca	ctt	cca	gtt	ctt	aaa	gga	agg	act	cct	gtc	caa	771
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tgc	tat	tct	gat	ttc	atg	aga	ggg	ttt	aga	gat	aga	ttt	gag	aat	ctc	819
Cys	Tyr	Ser	Asp	Phe	Met	Arg	Gly	Phe	Arg	Asp	Arg	Phe	Glu	Asn	Leu	
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cta	ggg	gac	acc	att	gtg	gaa	att	caa	gtc	ggg	atg	ggg	cca	gct	gga	867
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Glu	Leu	Arg	Tyr	Pro	Ser	Tyr	Pro	Glu	Lys	Asp	Gly	Val	Trp	Lys	Phe	
285					290					295					300	
cct	gga	att	ggg	gct	ttt	cag	tgt	tat	gac	aag	tac	atg	atc	agt	agc	963
Pro	Gly	Ile	Gly	Ala	Phe	Gln	Cys	Tyr	Asp	Lys	Tyr	Met	Ile	Ser	Ser	
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ctg caa tca gcc aag gcg ata ttc gag gac aag ggt gtt aag att tca Leu Gln Ser Ala Lys Ala Ile Phe Glu Asp Lys Gly Val Lys Ile Ser 385 390 395	1203
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gca cct gag aag ttg gtt agg caa gtg gct tta gca act cag gaa gct Ala Pro Glu Lys Leu Val Arg Gln Val Ala Leu Ala Thr Gln Glu Ala 465 470 475	1443
caa gtt cca ctt gct ggg gag aat gca ttg cca cga tac gat gat tat Gln Val Pro Leu Ala Gly Glu Asn Ala Leu Pro Arg Tyr Asp Asp Tyr 480 485 490	1491
gca cat gaa cag atc ctt caa gca tcc tca ttg aat atc aac gat caa Ala His Glu Gln Ile Leu Gln Ala Ser Ser Leu Asn Ile Asn Asp Gln 495 500 505	1539
tca ggt gat aga gag atg tgc gcg ttt aca tat ttg agg atg aat cct Ser Gly Asp Arg Glu Met Cys Ala Phe Thr Tyr Leu Arg Met Asn Pro 510 515 520	1587
gac cta ttc cat cct gat aac tgg agg cga ttc gtt gcc ttc gtg aag Asp Leu Phe His Pro Asp Asn Trp Arg Arg Phe Val Ala Phe Val Lys 525 530 535 540	1635
aaa atg aaa gaa gga aaa gac gca aac aaa tgc cgg gaa caa gta gag Lys Met Lys Glu Gly Lys Asp Ala Asn Lys Cys Arg Glu Gln Val Glu 545 550 555	1683

agg gag gca gag cat ttc gtg cat ata act cag ccg tta gtg caa gaa , 1731
 Arg Glu Ala Glu His Phe Val His Ile Thr Gln Pro Leu Val Gln Glu
 560 565 570

gct gca gct gcc ctc atg cac taagcaaatg gttgtcaaat agtactgtaa 1782
 Ala Ala Ala Ala Leu Met His
 575

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Ser Ser Ala Thr Ser Ala Met Trp Arg Thr Pro Met Thr Asn Leu Lys
 35 40 45

Val Ser Val Gln Lys Thr Gly Thr Glu Ile Asp Arg Val Ser Pro Ser
 50 55 60

Pro Ser Pro Pro Met Ser Pro Met Met Gly Gly Gly Met Arg Pro Asp
 65 70 75 80

Leu Leu Ala Cys Gln Ala Leu Met Glu Ala Gln Val Asp Glu Val Val
 85 90 95

Glu Arg Glu Tyr Lys Val Arg Asn Ser Ser Glu Lys Glu Lys Gly Val
 100 105 110

Pro Val Phe Val Met Met Pro Leu Asp Ser Val Lys Met Asp His Thr
 115 120 125

Val Asn Arg Lys Lys Ala Met Asn Ala Ser Leu Gln Ala Leu Lys Ser
 130 135 140

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Ala Gly Val Glu Gly Ile Met Met Asp Val Trp Trp Gly Leu Val Glu
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Arg Asp Ala Pro Gly Glu Tyr Asn Trp Gly Gly Tyr Ala Glu Leu Met
165 170 175

Glu Met Ala Lys Lys His Gly Leu Lys Val Gln Ala Val Met Ser Phe
180 185 190

His Gln Cys Gly Gly Asn Val Gly Asp Ser Cys Thr Ile Pro Leu Pro
195 200 205

Arg Trp Val Val Glu Glu Met Glu Lys Asp Pro Asp Leu Ala Tyr Thr
210 215 220

Asp Gln Trp Gly Arg Arg Asn Phe Glu Tyr Val Ser Leu Gly Cys Asp
225 230 235 240

Thr Leu Pro Val Leu Lys Gly Arg Thr Pro Val Gln Cys Tyr Ser Asp
245 250 255

Phe Met Arg Gly Phe Arg Asp Arg Phe Glu Asn Leu Leu Gly Asp Thr
260 265 270

Ile Val Glu Ile Gln Val Gly Met Gly Pro Ala Gly Glu Leu Arg Tyr
275 280 285

Pro Ser Tyr Pro Glu Lys Asp Gly Val Trp Lys Phe Pro Gly Ile Gly
290 295 300

Ala Phe Gln Cys Tyr Asp Lys Tyr Met Ile Ser Ser Leu Gln Gly Ala
305 310 315 320

Ala Glu Ala Phe Gly Lys Pro Glu Trp Gly His Thr Gly Pro Thr Asp
325 330 335

Ala Gly Gln Tyr Asn Asn Trp Pro Glu Asp Thr Asn Phe Phe Lys Lys
340 345 350

Glu Gly Gly Gly Trp Asp Ser Gln Tyr Gly Glu Phe Phe Leu Thr Trp
355 360 365

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